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Research Article

Detection, characterization of G × E interaction for pod yield in ABLs of *Arachis hypogaea* L. using AMMI and GGE biplot models

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Background: Groundnut seed yield varies considerably across environments due to genotype × environment (G × E) interactions, making the identification of high-yielding and stable genotypes essential for effective cultivar selection. Understanding G × E interactions across diverse agroclimatic environments is therefore important for identifying promising genotypes and suitable testing environments.

Methods: The study was conducted across two agroclimatic zones of Karnataka (Zones 4 and 5). During kharif 2024, twenty-nine genotypes comprising ten NRCG lines, sixteen DG lines and three checks (KCG 6, TMV 2 and GKVK 27) were evaluated at GKVK, Bengaluru, using a randomized complete block design (RCBD). Based on per se performance for pod yield and associated traits, seven superior genotypes were selected for further evaluation. During summer 2025, ten genotypes comprising seven DG lines and three checks were evaluated in an RCBD with three replications across three locations. AMMI and GGE biplot analyses were employed to assess G × E interactions, genotype stability and the discriminativeness and representativeness of test environments.

Results: AMMI analysis revealed significant G × E interactions, indicating differential responses of genotypes across environments. The first two principal components accounted for a major proportion of the interaction variation. AMMI biplot analysis identified DG 16 as a high-performing genotype for oil content with moderate stability. GGE biplot analysis identified GKVK 27 as the most desirable genotype for pods plant^{-1} and pod yield plant^{-1}, whereas DG 16 showed desirable performance for oil content. The discriminativeness and representativeness analysis identified Pavagada as the most discriminating and representative test environment for pods plant^{-1}, while Chinthamani was identified as the most suitable test environment for pod yield plant^{-1}.

Conclusion: The study demonstrated substantial G × E interaction for the evaluated groundnut traits and highlighted the importance of multi-environment testing for reliable genotype selection. GKVK 27 showed desirable performance for pods plant^{-1} and pod yield plant^{-1}, while DG 16 was promising for oil content with moderate stability. Pavagada and Chinthamani were identified as useful test environments for pods plant^{-1} and pod yield plant^{-1}, respectively. These

findings can support the selection of promising groundnut genotypes and optimization of testing environments under diverse agroclimatic conditions of Karnataka.

Keywords: *Groundnut, AMMI, GGE biplot, stability analysis, ideal genotype*

Introduction

Groundnut (*Arachis hypogaea* L.), commonly known as peanut, is an important food and oilseed crop cultivated extensively across tropical and subtropical regions of the world. It is a self-pollinated, allotetraploid (2n = 4x = 40) member of the Fabaceae, often referred to as the "king of oilseeds" due to its high oil and protein content. The crop originated in South America through hybridization between *A. duranensis* (A genome) and *A. ipaensis* (B genome), followed by natural chromosome duplication (Bertioli et al., 2016), while Africa is considered a secondary centre of diversity (Vavilov, 1951). Groundnut kernels contain 48-50% oil, 25-28% protein, and a wide range of essential minerals and bioactive compounds, contributing to their nutritional and economic significance (Sanni et al., 2024). Worldwide, the crop occupies 309.21 lakh ha with a production of 542.73 lakh tonnes (FAOSTAT, 2025). India ranks as the second-largest producer after China, cultivating groundnut on 57.54 lakh hectares and producing 118.96 lakh tonnes with a productivity of 2067 kg ha^{-1}. Major groundnut-growing states include Gujarat, Rajasthan, and Madhya Pradesh (Anonymous, 2024). Despite its importance, productivity remains suboptimal due to the predominance of rainfed farming and inconsistent varietal performance across diverse production environments. Pod yield in groundnut is a complex polygenic trait highly influenced by environmental variation, resulting in significant genotype × environment interaction (GEI) that hampers the identification of stable, high-yielding cultivars (Patil et al., 2014). Multivariate tools such as AMMI (Gauch & Zobel, 1988) and GGE biplot analysis (Yan & Kang, 2002) are therefore used to effectively dissect GEI and identify genotypes with superior performance and broad adaptability, which is essential for developing advanced breeding lines suited to diverse agro-ecological conditions.

Materials and Methods

The details of the experimental sites, plant materials, experimental design, evaluation protocol and statistical analyses used in the study are described below.

Experimental material

The study initially included 29 groundnut genotypes, comprising 16 DG lines from the University of Agricultural Sciences, Dharwad, 10 NRCG lines obtained from ICAR-DGR (formerly NRCG), Junagadh and 3 checks (KCG 6, TMV 2, GKVK 27) (Table 1). These genotypes were evaluated during Kharif 2024 at the K-block, GKVK, Bengaluru, using a Randomized Complete Block Design (RCBD) with two replications. Based on *per se* performance for pod yield and associated traits, seven superior genotypes were selected for stability analysis. In the following season (summer 2025), these seven genotypes, along with three check varieties (Table 2), were evaluated across three locations (Table 3).

Table 1. List of groundnut genotypes used in the study

Sl. No.	Genotypes	Sl. No.	Genotypes
1	NRCG 13914	16	DG 6
2	NRCG 10314	17	DG 7
3	NRCG 5521	18	DG 8
4	NRCG 117	19	DG 9
5	NRCG 10295	20	DG 10
6	NRCG 94	21	DG 11
7	NRCG 14721	22	DG 12
8	NRCG 13947	23	DG 13
9	NRCG 10382	24	DG 14
10	NRCG 14010	25	DG 15
11	DG 1	26	DG 16
12	DG 2	27	KCG 6
13	DG 3	28	TMV 2
14	DG 4	29	GKVK 27
15	DG 5		-

Table 2. List of selected genotypes used for stability analysis across three locations

Sl. No.	Genotypes	Source	Code
1	DG 9	ABL	G1
2	DG 10	ABL	G2
3	DG 11	ABL	G3
4	DG 12	ABL	G4
5	DG 14	ABL	G5
6	DG 15	ABL	G6
7	DG 16	ABL	G7
8	KCG 6	Check variety	G8
9	TMV 2	Check variety	G9
10	GKVK 27	Check variety	G10

Table 3. Locations, Agroclimatic Zones, and Geographical Coordinates of Experimental Sites

Location	Agroclimatic zone	Altitude (m MSL)	Latitude (N)	Longitude (E)
GKVK, Bengaluru	Zone 5	930	12°58′	77°35′
CoS, Chintamani	Zone 5	924	13°40′	78°06′
ARS, Pavagada	Zone 4	768	14°05′	77°28′

Data collection

Observations were recorded from five randomly selected plants per replication at each location. The traits recorded were days to 50% flowering, primary branches plant^{-1}, plant height (cm), number of pods plant^{-1}, pod yield plant^{-1} (g), kernel yield plant^{-1} (g), shelling percentage, 100-kernel weight (g), sound mature kernel (%), oil content (%).

Statistical analysis

The replication-wise mean values of genotypes were subjected to analysis of variance (ANOVA) for RCBD (Panse & Sukhatme, 1985) to assess the significance of differences among genotypes within each location. Total variability was partitioned into components due to replications, genotypes, and experimental error. Pooled ANOVA across locations was performed following Sundara Raj et al. (1972) to evaluate the effects of genotypes, locations, and genotype × location interaction (GLI). To further characterize genotype × location interaction (GLI), the Additive Main Effects and Multiplicative Interaction (AMMI) model was applied (Gauch & Zobel, 1988). Genotypic and location main effects were estimated using ANOVA, followed by partitioning of GLI through interaction principal component (IPC) analysis. The model used was:

$$\boldsymbol{Y_{ij}} = \mu + \boldsymbol{g_i} + \boldsymbol{e_{j+}} \sum_{\boldsymbol{k=1}}^{\boldsymbol{n}} \boldsymbol{\lambda_k \alpha_{ik} \gamma_{jk}} + \boldsymbol{\varepsilon_{ij}}$$

Where, Y_{ij} is the quantitative trait mean of ith genotype in the jth location, μ is the experimental quantitative trait mean, g_i and e_j are the ith genotype and jth location mean deviation from experimental quantitative trait mean values, respectively. λ_k is the square root of the value of the kth IPC axis, α_{ik} and γ_{jk} are the interaction principal components (IPC) scores for kth IPC of the ith genotype and jth location, respectively and ε_{ij} is the residual. All the analyses were implemented using R software *version* 4.5.1.

GGE biplot analysis

Genotype + Genotype × Environment (GGE) biplot analysis (Yan et al., 2000) was employed to visually interpret genotype × location interaction (GLI) patterns and assess genotype stability. The GGE model is expressed as:

$$\boldsymbol{Y_{ij} - Y_i = \lambda_1 \alpha_{i1} \gamma_{i1} + \lambda_2 \alpha_{i2} \gamma_{j2} + \varepsilon_{ij}}$$

Where, Yij is the trait mean of ith genotype in the jth location, Y_i is trait mean of all the genotypes in the jth location, λ_1 and λ_2 are square root of eigen values of first and second IPC axes, 1 and 2, α_{i1} and α_{i2} are scores of the first and second IPC, respectively, for the ith genotype and γ_{ij} and $\gamma_{ij}$are first and second IPCs respectively for jth location.

Among several approaches to interpret GGE biplots, the following views are most relevant (Segherloo et al., 2010):

1. **Discriminativeness *vs.* representativeness** of test environments, and
2**. Average Environment Coordinate (AEC) view** based on genotype-focused scaling for ranking genotypes relative to the ideal genotype.

Results and Discussion

To assess the per se performance of advanced breeding lines (ABL) of groundnut

The *per se* performance of 29 groundnut genotypes (ten NRCG lines, sixteen DG lines, and three checks) was evaluated using RCBD ANOVA for pod yield and associated traits. The analysis revealed highly significant mean squares ($p < 0.01$), indicating substantial variability among genotypes and confirming the suitability of the material for selection (Table 4). Seven DG ABLs (Advanced breeding lines) were selected based on them *per se* performance compared with the checks (KCG 6, TMV 2, and GKVK 27), particularly for number of pods plant^{-1}, pod yield plant^{-1} (g), kernel yield plant^{-1} (g), shelling percentage, oil content (%), and pod yield plot^{-1} (kg), demonstrating notable variability among the genotypes. These traits, being directly linked to productivity and quality, were used as the primary criteria for selecting superior genotypes.

Table 4. Estimates of mean sum of squares for pod yield and its attributing traits among 29 groundnut genotypes during *kharif* 2024

Source of variation	Df	PDN	PDY	KY	SP	OC	PDYP
Replication	1	0.001	0.11	0.10	0.0001	1.91	0.00079
Genotypes	28	89.00**	60.39**	27.92**	81.52**	21.42**	0.01344**
Error	28	0.19	0.05	0.19	0.19	0.45	0.00332

** Significant at P = 0.01
Df-degrees of freedom; PDN-Number of pods plant^{-1}; PDY-pod yield plant^{-1} (g); KY-Kernel yield plant^{-1} (g); SP-Shelling percentage; OC-Oil content (%); PDYP- pod yield plot^{-1} (kg)

To identify stable genotypes for pod yield and its components across two different agroclimatic zones of Karnataka:

Pooled ANOVA

In the pooled ANOVA, the total variation was partitioned into effects due to genotypes, locations, genotype × location interactions (GLI), and pooled error. From a breeding standpoint, the most critical components are the genotypic effects and GLI. In the present study, significant genotypic variation indicated ample scope for selecting superior lines, while the significant GLI component suggested differential performance of genotypes across environments. During Summer 2025, pod yield and its component traits were evaluated across three test locations. The pooled analysis revealed significant genotype effects for all traits, demonstrating inherent genetic variability. In addition, highly significant genotype × location interactions for every trait confirmed the strong influence of environmental factors on trait expression (Table 5). Similar findings of significant GEI for pod yield and related traits have been reported by Minimol et al. (2000), Dolinassou et al. (2016), Khan et al. (2021) and Kona et al. (2024).

AMMI model-based characterization of genotypes × location interaction

Standard additive ANOVA detects GEI only if the average of all (g–1) (e–1) contrasts is significant, and may miss large interactions for some contrasts. GEI is considered absent only if the GEI sum of squares for one degree of freedom is not significant (Gauch & Zobel, 1988). The AMMI model overcomes this limitation by combining additive ANOVA for main effects with multiplicative PCA, effectively detecting and characterizing GEI and identifying genotypes with stable performance across locations. In the present investigation, the AMMI analysis indicated significant differences among the genotypes as well as genotype × location interactions for yield and its related traits, highlighting the presence of genetic variability and the inconsistent performance of genotypes across different environments (Table 6). Patil et al. (2014) reported significant GEI for flowering, growth, yield, and quality traits in groundnut, while Purnomo and Rahmianna (2020) also observed significant GEI for pod number, pod yield, plant height, seed weight, and shelling percentage.

Table 5. Estimates of pooled mean sum of squares for pod yield and its attributing traits among ABLs of groundnut across three locations

Source of variation	Degrees of freedom	Days to 50% flowering	Primary branches plant^{-1}	Plant height (cm)	Number of pods plant^{-1}	Pod yield plant^{-1} (g)	Kernel yield plant^{-1} (g)	Shelling percentage	Sound mature kernel (%)	100-kernel weight (g)	Oil content (%)
Location	2	2.133**	15.44**	262.8**	217.74**	230.02**	80.73**	218.15**	20.32**	2.62**	90.17**
Replication	6	0.156	0.16	0.841	0.02	0.0084	0.040	0.913	0.589	0.018	0.314
Genotypes	9	6.983**	1.41**	10.65**	53.06**	93.6**	24.06**	11.87**	24.28**	142.40**	48.16**
Genotypes × Locations	18	1.257**	0.75**	6.90**	5.61**	13.4**	1.99**	31.64**	27.3**	3.56**	15.42**
Pooled error	54	0.291	0.075	0.49	0.04	0.045	0.018	0.661	0.254	0.033	0.035

*Significant at P = 0.05; ** Significant at P = 0.01

Table 6. AMMI ANOVA of groundnut ABLs evaluated across three locations for yield and its attributing traits

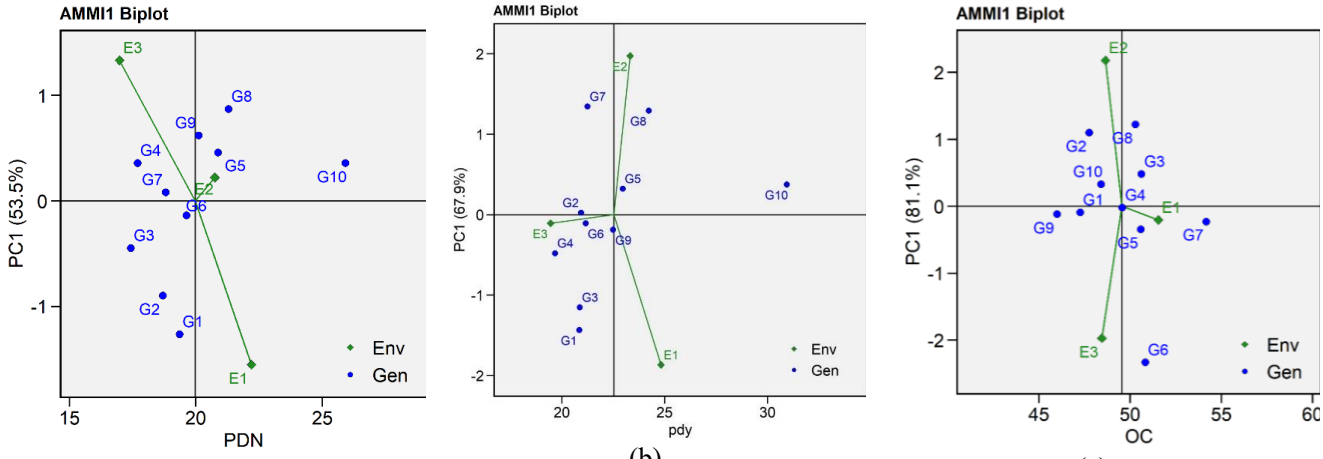
Source of variation	Degrees of freedom	Days to 50% flowering (MSS)	% variation	Primary branches plant^{-1} (MSS)	% variation	Plant height (cm) (MSS)	% variation	Number of pods plant^{-1} (MSS)	% variation	Pod yield plant^{-1} (g) (MSS)	% variation
Total	89	1.206	–	0.710	–	8.424	–	10.44	–	16.70	–
Replications	6	0.156	0.73	0.164	1.30	0.841	0.56	0.02	0.01	0.008	0.002
Genotypes (G)	9	6.983**	48.8	1.412**	16.72	10.65**	10.63	53.06**	42.73	93.60**	47.03
Locations (L)	2	2.133**	3.30	15.44**	40.64	262.8**	58.31	217.7**	38.96	230.0**	25.69
G × L	18	1.257**	17.53%	0.756**	17.92	6.90**	13.78	5.61**	9.04	13.44**	13.52
IPCA 1	10	1.824**	80.63% of G×L	1.207**	88.70% of G×L	9.30**	74.91% of G×L	5.40**	53.45% of G×L	16.40**	67.77% of G×L
IPCA 2	8	0.548**	19.36% of G×L	0.192**	11.29% of G×L	3.89**	25.08% of G×L	5.87**	46.54% of G×L	9.70**	32.06% of G×L
Residuals	54	0.291	12.19	0.077	5.50	0.49	2.93	0.042	0.20	0.042	0.12

Source of variation	Degrees of freedom	Kernel yield plant^{-1} (g) (MSS)	% variation	Shelling percentage (MSS)	% variation	100-kernel weight (g) (MSS)	% variation	Sound mature kernel (%) (MSS)	% variation	Oil content (%) (MSS)	% variation
Total	89	4.21	–	16.10	–	13.24	–	11.80	–	10.96	–
Replications	6	0.040	0.05	0.913	0.32	0.018	0.007	0.589	0.28	0.314	0.16
Genotypes (G)	9	24.06**	48.02	11.87**	6.19	142.4**	90.43	24.28**	17.30	48.16**	36.95
Locations (L)	2	80.73**	35.80	218.1**	25.31	2.62**	0.37	20.32**	3.21	90.17**	15.37
G × L	18	1.99**	7.94	31.64**	33.05	3.56**	4.52	27.39**	39.05	15.42**	23.67
IPCA 1	10	2.25**	62.79% of G×L	41.54**	72.93% of G×L	3.74**	58.42% of G×L	29.62**	60.07% of G×L	22.53**	81.14% of G×L
IPCA 2	8	1.66**	37.20% of G×L	19.27**	27.06% of G×L	3.33**	41.57% of G×L	24.61**	39.92% of G×L	6.54**	18.85%
Residuals	54	0.018	0.21	0.661	2.07	0.033	0.13	0.254	1.08	0.035	0.16

Additive Main Effects and Multiplicative Interaction (AMMI) biplots for assessing stability

Additive Main Effects and Multiplicative Interaction 1 (AMMI 1) biplot:

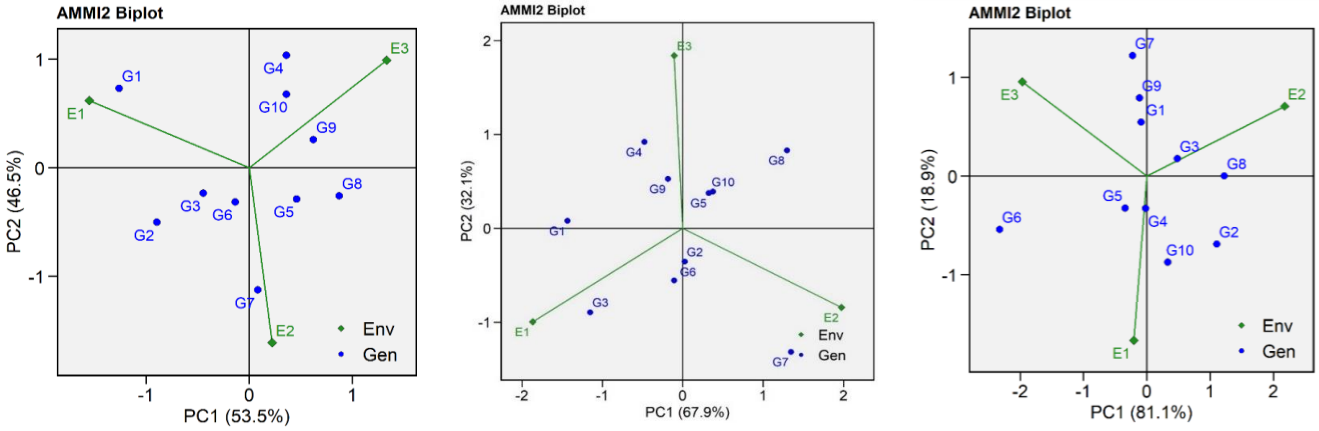
In AMMI 1 biplot analysis, the mean performance of traits is plotted along the X-axis, while the IPCA1 scores are represented on the Y-axis, enabling a combined evaluation of both yield potential and stability of genotypes across environments. Genotypes located near the zero line of the IPCA1 axis are stable and the genotypes that fall on the right side show high trait values. For the number of pods plant^{-1}, the genotypes G6 (DG 15, 19.63), G7 (DG 16, 18.8) had a moderate number of pods and were more stable**.** In contrast G10 (GKVK 27, 25.9) had a greater number of pods and moderately stable (Figure 1a). The genotypes G2 (DG 10, 20.94), G6 (DG 15, 21.16), G9 (TMV 2, 22.49) recorded stable performance with average trait mean for pod yield plant^{-1} (g) and genotype G10 (GKVK 27, 30.94) exhibited above average trait mean and relatively less stable, the genotype G5 (DG 14, 22.96), G8 (KCG 6, 24.23 had comparable trait mean with G9 (TMV 2) but were less stable (Figure 1b). For oil content (%), G7 (DG 16; 54.48%) showed the highest oil content with moderate stability. G6 (DG 15; 50.90%), G3 (DG 11; 50.65%) and G8 (KCG 6; 50.32%) had above-average means but lower stability. G4 (DG 12; 49.71%) and G5 (DG 14; 50.61%) were stable with near-average means. G1 (DG 9; 47.37%) and G10 (GKVK 27; 48.43%) showed average means with stability, while G9 (TMV 2; 46.06%) recorded a lower mean but remained stable. G2 (DG 10; 47.82%) showed below-average mean and lower stability (Figure 1c). AMMI 1 biplots were also employed by Firdisa et al. (2024), Haque et al. (2024), and Kona et al. (2024) to identify stable and high-yielding genotypes, wherein comparable findings were reported.



(a) (b) (c)

Figure 1. AMMI 1 biplot for (a) Number of pods plant^{-1}; (b) Pod yield plant^{-1} (g) and (c) Oil content (%)

Additive main effects and multiplicative interaction 2 (AMMI 2) biplot



(a) (b) (c)

Figure 2. AMMI 2 biplot for (a) Number of pods plant^{-1}; (b) Pod yield plant^{-1} (g) and (c) Oil content (%)

The AMMI-2 biplot effectively illustrates the genotype × environment interaction, enabling a comprehensive understanding of genotype responses across test environments. Unlike AMMI-1, AMMI-2 incorporates the first two

interaction principal components (IPCA1 and IPCA2), thereby explaining a greater proportion of the interaction variation. In such biplots, genotypes positioned close to the origin are regarded as highly stable, whereas those located farther from the origin are considered less stable. For number of pods plant^{-1}, G6 (DG 15) and G3 (DG 11) showed broad adaptation. At the same time, G1 (DG 9), G9 (TMV 2) and G7 (DG 16) exhibited specific adaptation (Figure 2a). For pod yield plant^{-1} (g), G5 (DG 14), G2 (DG 10), G6 (DG 15) and G10 (GKVK 27) were broadly adapted, whereas G7 (DG 16) and G3 (DG 11) showed narrow adaptation (Figure 2b). Regarding oil content (%), G4 (DG 12), G5 (DG 14) and G3 (DG 11) were broadly adapted, while G7 (DG 16) and G8 (KCG 6) showed narrow adaptation (Figure 2c). The results confirm the effectiveness of the AMMI-2 biplot in identifying stable and widely adapted genotypes across environments. Genotypes DG 15 and DG 11 exhibited consistent broad adaptability for number of pods plant^{-1} and DG 12 and DG 14 for oil content (%), indicating their potential as stable donors in groundnut breeding programs. Similar findings on the utility of AMMI biplots for stability analysis under variable environments were reported by Dolinassou et al. (2016) and Kebede & Getahun (2017).

GGE Biplot analysis of GEI patterns

Discriminativeness vs. representativeness:

An ideal test environment should be both highly discriminative, clearly differentiating genotypes, and representative, reflecting mean performance across locations. In a GGE biplot, the environment vector's length indicates discriminating ability, with longer vectors showing greater differentiation. Representativeness is measured by the angle between the vector and the Average Environment Coordinate (AEC) abscissa; smaller angles indicate higher representativeness. Thus, an environment with a long vector and a small angle with the AEC abscissa is most suitable for identifying superior and stable genotypes. Environment E3 (ARS, Pavagada) was ideal for selecting genotypes for pods per plant, being both highly discriminating (long vector) and representative (small angle with AEC) (Figure 3a). For pod yield plant^{-1} (g), E2 (CoS, Chintamani) showed high discriminating ability, while E3 (ARS, Pavagada) was representative, making these environments suitable for selecting broadly adapted genotypes (Figure 3b). For oil content (%), although E3 was highly discriminative, its low representativeness limited its suitability. In contrast, E1 (GKVK) was both discriminative and representative, making it the most suitable environment for oil content (Figure 3c). Similar findings were reported by Kebede & Getahun (2017), Okori et al. (2019), and Sendekie et al. (2020), who highlighted the usefulness of GGE biplots in identifying test environments with high discriminating ability and strong representativeness. These studies confirmed that such environments are most effective for selecting superior genotypes with broad adaptability across diverse conditions.

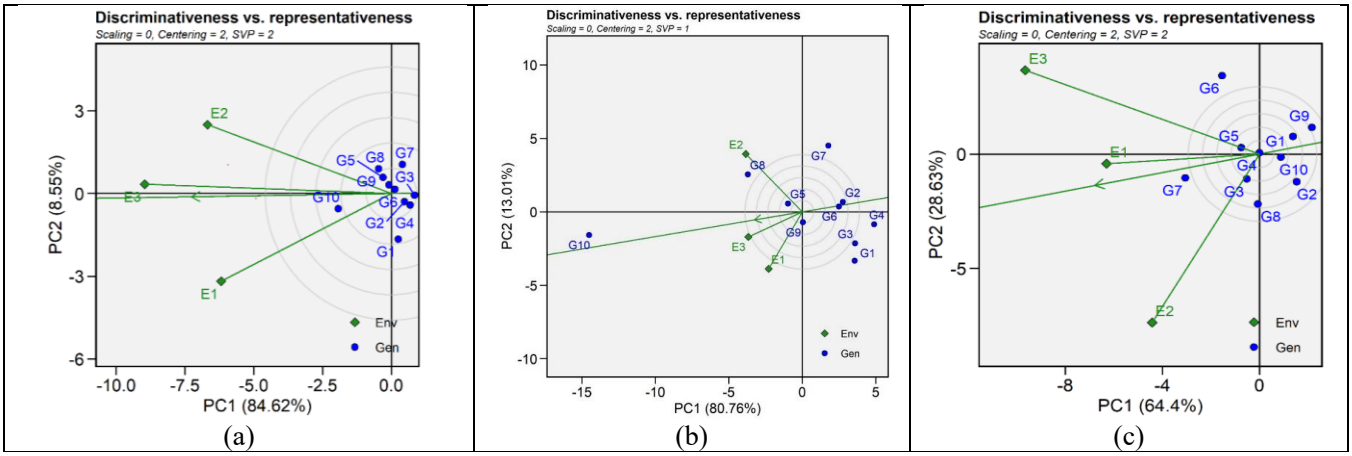


Figure. 3. Discriminativeness *vs*. representativeness biplot for (a) Number of pods plant^{-1}; (b) Pod yield plant^{-1} (g) and (c) Oil content (%)

Ranking of genotypes relative to 'ideal genotype'

The genotype ranking biplot identifies an ideal genotype by jointly considering mean performance and stability, represented by a point on the Average Environment Axis within the innermost concentric circle. Genotypes closer to this point exhibit higher mean performance and greater stability, with projection onto the Average Environment Coordinate indicating mean performance and distance from the origin reflecting stability. Accordingly, genotypes located in the inner concentric circles are considered more desirable than those farther away. For pods plant^{-1}, G10 (GKVK 27) was identified as the ideal genotype across the three locations, positioned closest to the origin and within the innermost circle (Figure

4a). Genotypes G8 (KCG 6), G5 (DG 14), and G9 (TMV 2) were classified as near-ideal, lying adjacent to the innermost circle for pod yield plant^{-1} (Figure 4b). For oil content (%), G7 (DG 16) was identified as the ideal genotype, while G3 (DG 11) and G5 (DG 14) were near-ideal (Figure 4c). The present findings support the effectiveness of the 'ideal genotype' approach, previously demonstrated by Premika et al. (2024) and Esan et al. (2023), for selecting genotypes that exhibit both superior performance and stability across varied environments.

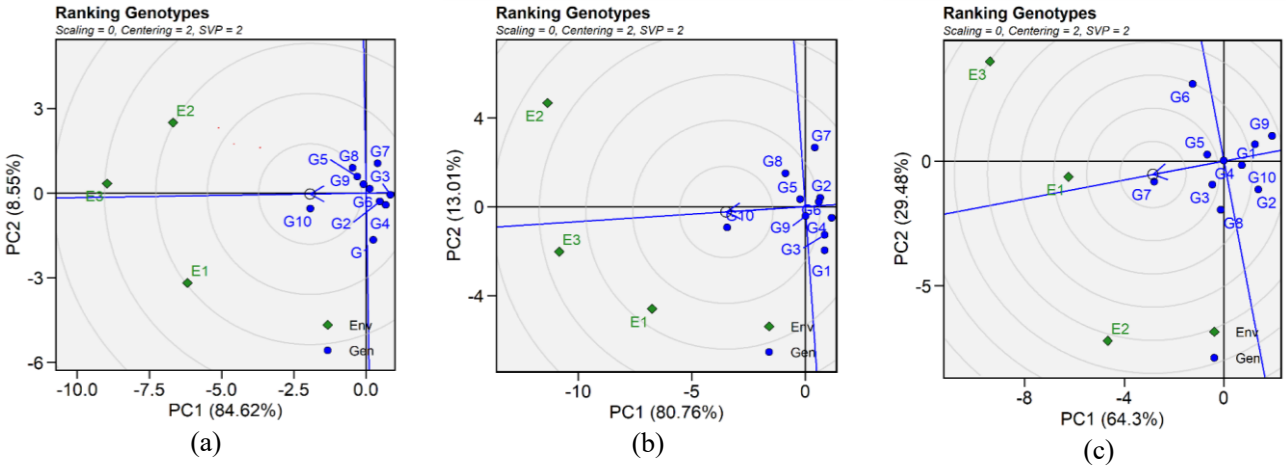


Figure. 4. Ranking of genotypes relative to ideal one for (a) Number of pods plant^{-1}; (b) Pod yield plant^{-1} (g) and (c) Oil content (%)

Conclusion

DG 16 was identified as a moderately stable, high-performing genotype for oil content (%) across multiple environments, while GKVK 27 showed broad adaptability for number of pods plant^{-1} and for pod yield plant^{-1}. These genotypes have strong potential for use in future groundnut breeding programs aimed at enhancing productivity, stability, and quality under diverse agroclimatic conditions.

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Author contributions

Siddam Divya: Scholar who conducted the research and developed the manuscript. Priyadarshini S K: Major advisor, Guidance, manuscript editing, technical supervision, implementation of the experiment at Chintamani. Marappa N: Advisory member, implementation of the experiment at UAS GKVK, Bangalore. Syed Mazar Ali: implementation of the experiment at ARS, Pavagada. Laxmi Patil: providing Material for the experiment. Venkataravana P: Technical guidance and facilitating the research activities at Chintamani campus.

Conflict of interest

The authors declare no conflict of interest. The patent application (No. 202641031666) was filed by the same research team; however, no commercial funding was received for this research.

Ethics approval

Not applicable.

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AI tool usage declaration

The authors used Grammarly AI tool for improving grammar, language clarity, and spelling.

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